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**RAW SEQUENCE LISTING**  
PATENT APPLICATION: US/09/612,925D

DATE: 03/19/2003  
TIME: 11:57:41

Input Set : N:\Crf3\RULE60\09612925.raw.txt  
Output Set: N:\CRF4\03192003\I612925D.raw

**SEQUENCE LISTING**

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: DUARTE CANO, C. A.  
6 GUILL N NIETO, G. E.  
7 MART N DUNN, A. M.  
8 ALVAREZ ACOSTA, A.  
9 CARPIO MU%OZ, E. L.  
10 QUINTANA V. D.  
11 G MEZ RODR GUEZ, C. E.  
12 SILVA RODR GUEZ, R. C.  
13 NAZ BAL G LVEZ, C.  
14 LEAL ANGULO, M. J.

16 (ii) TITLE OF INVENTION: System for the expression of heterologous  
17 antigens as fusion proteins

19 (iii) NUMBER OF SEQUENCES: 21

21 (iv) CORRESPONDENCE ADDRESS:

22 (A) ADDRESSEE: Lackenbach Siegel Marzullo Aronson & Greenspan  
23 (B) STREET: One Chase Road  
24 (C) CITY: Scarsdale  
25 (D) STATE: New York  
26 (E) COUNTRY: U.S.  
27 (F) ZIP: 10583

29 (v) COMPUTER READABLE FORM:

30 (A) MEDIUM TYPE: Floppy disk 3.5'' (1.4 MB).  
31 (B) COMPUTER: Compatible PC IBM (80486, 8 M Ram).  
32 (C) OPERATING SYSTEM: Windows 95.  
33 (D) SOFTWARE: Word Perfect 5.0 for Windows 95.

35 (vi) CURRENT APPLICATION DATA:

C--> 36 (A) APPLICATION NUMBER: US/09/612,925D  
C--> 37 (B) FILING DATE: 10-Jul-2000  
W--> 43 (C) CLASSIFICATION: 435

40 (vii) PRIOR APPLICATION DATA:

41 (A) APPLICATION NUMBER: US/08/930,917A  
42 (B) FILING DATE: 16-Sep-1997  
44 (A) APPLICATION NUMBER: PCT/CU97/00001  
45 (B) FILING DATE: 17-Jan-1997

47 (viii) ATTORNEY/AGENT INFORMATION:

48 (A) NAME: HENRY A. MARZULLO, JR.  
49 (B) REGISTRATION NUMBER: 20,910  
50 (C) REFERENCE/DOCKET NUMBER: P-13

52 (ix) TELECOMMUNICATION INFORMATION:

53 (A) TELEPHONE: (914) 723-4300  
54 (B) TELEFAX: (914) 723-4301

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57 (2) INFORMATION FOR SEQ ID NO: 1:

59 (i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 47 Amino acid residues

61 (B) TYPE: Amino acid

62 (C) STRANDEDNESS: Unknown

63 (D) TOPOLOGY: Unknown

65 (ii) MOLECULE TYPE: Peptide

67 (iii) HYPOTHETICAL: No

69 (iv) ANTI-SENSE: No

W--&gt; 71 (v) FRAGMENT TYPE: -N Terminal fragment

73 (vi) ORIGINAL SOURCE:

74 (A) ORGANISM: Neisseria meningitidis

75 (B) STRAIN: B:4:P1.15

77 (vii) IMMEDIATE SOURCE:

78 (A) LIBRARY: Genomic

79 (B) CLONE: P64K

81 (ix) FEATURE:

82 (D) OTHER INFORMATION: First 47 amino acids of the recombinant protein  
83 of Neisseria meningitidis P64K.

85 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

86 Met Leu Asp Lys Arg Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile

87 1 5 10 15

88 Gly Gly His Glu Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly

89 20 25 30

90 Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Glu Thr Asp

91 35 40 45

93 (2) INFORMATION FOR SEQ ID NO: 2:

94 (i) SEQUENCE CHARACTERISTICS:

95 (A) LENGTH: 29 base pairs

96 (B) TYPE: Nucleic acid

97 (C) STRANDEDNESS: Unknown

98 (D) TOPOLOGY: Unknown

100 (ii) MOLECULE TYPE: Other nucleic acid

101 (A) DESCRIPTION: Synthetic oligonucleotide

103 (iii) HYPOTHETICAL: No.

105 (iv) ANTI-SENSE: No

W--&gt; 107 (v) FRAGMENT TYPE: -N Terminal fragment

109 (vi) ORIGINAL SOURCE:

110 (A) ORGANISM: Neisseria meningitidis

111 (B) STRAIN: B:4:P1.15

113 (vii) IMMEDIATE SOURCE:

114 (A) LIBRARY: Genomic

115 (B) CLONE: P64K

117 (ix) FEATURE:

118 (A) NAME/KEY: 1573

119 (D) OTHER INFORMATION: Primer 5' for PCR amplification of the first  
120 44 amino acids of the recombinant protein of Neisseria  
121 meningitidis P64K.

123 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

## RAW SEQUENCE LISTING

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Input Set : N:\Crf3\RULE60\09612925.raw.txt  
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124 TTCCATGGTA GATAAAAGAA TGGCTTTAG 29  
 126 (2) INFORMATION FOR SEQ ID NO: 3:  
 128 (i) SEQUENCE CHARACTERISTICS:  
 129 (A) LENGTH: 29 base pairs  
 130 (B) TYPE: Nucleic acid  
 131 (C) STRANDEDNESS: Unknown  
 132 (D) TOPOLOGY: Unknown  
 134 (ii) MOLECULE TYPE: Other nucleic acid  
 135 (A) DESCRIPTION: Synthetic oligonucleotide  
 137 (iii) HYPOTHETICAL: No.  
 139 (iv) ANTI-SENSE: No  
**W--> 141 (v) FRAGMENT TYPE: -C Terminal fragment**  
 142 (vi) ORIGINAL SOURCE:  
 143 (A) ORGANISM: Neisseria meningitidis  
 144 (B) STRAIN: B:4:P1.15  
 146 (vii) IMMEDIATE SOURCE:  
 147 (A) LIBRARY: Genomic  
 148 (B) CLONE: P64K  
 150 (ix) FEATURE:  
 151 (A) NAME/KEY: 1575  
 152 (D) OTHER INFORMATION: Primer 3' for PCR amplification of the first  
 153 47 amino acids of the recombinant protein of Neisseria  
 154 meningitidis P64K.  
 156 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 157 TTTCTAGATC CAAAGTAATC AGGGTATCG 29  
 159 (2) INFORMATION FOR SEQ ID NO: 4:  
 161 (i) SEQUENCE CHARACTERISTICS:  
 162 (A) LENGTH: 26 base pairs  
 163 (B) TYPE: Nucleic acid  
 164 (C) STRANDEDNESS: Unknown  
 165 (D) TOPOLOGY: Unknown  
 167 (ii) MOLECULE TYPE: Other nucleic acid  
 168 (A) DESCRIPTION: Synthetic oligonucleotide  
 170 (iii) HYPOTHETICAL: No  
 172 (iv) ANTI-SENSE: No  
**W--> 174 (v) FRAGMENT TYPE: -C Terminal fragment**  
 176 (vi) ORIGINAL SOURCE:  
 177 (A) ORGANISM: Neisseria meningitidis  
 178 (B) STRAIN: B:4:P1.15  
 180 (vii) IMMEDIATE SOURCE:  
 181 (A) LIBRARY: Genomic  
 182 (B) CLONE: P64K  
 184 (ix) FEATURE:  
 185 (A) NAME/KEY: Primer 2192  
 186 (D) OTHER INFORMATION: Primer 3' for PCR amplification of the first  
 187 120 amino acids of the recombinant protein of Neisseria  
 188 meningitidis P64K  
 190 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
 191 GGCGGTTCTG CCGATTAAGG ATCCGA 26

**RAW SEQUENCE LISTING**  
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**Output Set: N:\CRF4\03192003\I612925D.raw**

193 (2) INFORMATION FOR SEQ ID NO: 5:  
 195       (i) SEQUENCE CHARACTERISTICS:  
 196           (A) LENGTH: 146 base pairs  
 197           (B) TYPE: Nucleic acid  
 198           (C) STRANDEDNESS: Unknown  
 199           (D) TOPOLOGY: Unknown  
 201       (ii) MOLECULE TYPE: Other nucleic acid  
 202           (A) DESCRIPTION: Fragment amplified by PCR  
 204       (iii) HYPOTHETICAL: Yes  
 206       (iv) ANTI-SENSE: No  
 208           (v) FRAGMENT TYPE: -N-terminal fragment  
 210       (vi) ORIGINAL SOURCE:  
 211           (A) ORGANISM: Neisseria meningitidis  
 212           (B) STRAIN: B:4:P1.15  
 214       (vii) IMMEDIATE SOURCE:  
 215           (A) LIBRARY: Genomic  
 216           (B) CLONE: P64K  
 218       (ix) FEATURE:  
 219           (D) OTHER INFORMATION: Fragment derived from the first 47 amino acids  
 220 of the recombinant protein of Neisseria meningitidis P64K,  
 221 containing a NcoI site at the position 3 to 8 and a XbaI site  
 222 at the position 139 to 144  
 224       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
 225 TTCCATGGTA GATAAAAGAA TGGCTTAGT TGAATTGAAA GTGCCCGACA TTGGCGGACA 60  
 227 CGAAAATGTA GATATTATCG CGGTTGAAGT AAACGTGGGC GACACTATTG CTGTGGACGA 120  
 229 TACCCTGATT ACTTTGGATC TAGAAA 146  
 232 (2) INFORMATION FOR SEQ ID NO: 6:  
 234       (i) SEQUENCE CHARACTERISTICS:  
 235           (A) LENGTH: 47 Amino acid residues  
 236           (B) TYPE: Amino acid  
 237           (C) STRANDEDNESS: Unknown  
 238           (D) TOPOLOGY: Unknown  
 240       (ii) MOLECULE TYPE: Peptide  
 242       (iii) HYPOTHETICAL: No  
 244       (iv) ANTI-SENSE: No  
 W--> 246       (v) FRAGMENT TYPE: -N Terminal fragment  
 248       (vi) ORIGINAL SOURCE:  
 249           (A) ORGANISM: Neisseria meningitidis  
 250           (B) STRAIN: B:4:P1.15  
 252       (vii) IMMEDIATE SOURCE:  
 253           (A) LIBRARY: Genomic  
 254           (B) CLONE: P64K  
 256       (ix) FEATURE:  
 257           (D) OTHER INFORMATION: Stabilizer derived from the first 47 amino  
 258 acids of the recombinant protein of Neisseria meningitidis P64K,  
 259 containing the following changes: L2 V2; E45 D45; T46 L46; D47 E47.  
 261       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
 262 Met Val Asp Lys Arg Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile  
 263 1                   5                   10                   15

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/612,925D

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264 Gly Gly His Glu Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly

265 20 25 30

266 Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Asp Leu Glu

267 35 40 45

269 (2) INFORMATION FOR SEQ ID NO: 7:

271 (i) SEQUENCE CHARACTERISTICS:

272 (A) LENGTH: 16 base pairs

273 (B) TYPE: Nucleic acid

274 (C) STRANDEDNESS: Unknown

275 (D) TOPOLOGY: Unknown

276 (ii) MOLECULE TYPE: Other nucleic acid

277 (A) DESCRIPTION: Synthetic oligonucleotide

279 (iii) HYPOTHETICAL: No.

281 (iv) ANTI-SENSE: No

W--&gt; 283 (v) FRAGMENT TYPE: -N Terminal fragment

285 (vi) ORIGINAL SOURCE:

286 (A) ORGANISM: Neisseria meningitidis

287 (B) STRAIN: B:4:P1.15

289 (vii) IMMEDIATE SOURCE:

290 (A) LIBRARY: Genomic

291 (B) CLONE: P64K

293 (ix) FEATURE:

294 (A) NAME/KEY: 1576

295 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7 :

296 CTAGATTGAT TATCAG

16

298 (2) INFORMATION FOR SEQ ID NO: 8:

300 (i) SEQUENCE CHARACTERISTICS:

301 (A) LENGTH: 16 base pairs

302 (B) TYPE: Nucleic acid

303 (C) STRANDEDNESS: Unknown

304 (D) TOPOLOGY: Unknown

306 (ii) MOLECULE TYPE: Other nucleic acid

307 (A) DESCRIPTION: Synthetic oligonucleotide

309 (iii) HYPOTHETICAL: No

311 (iv) ANTI-SENSE: No

W--&gt; 313 (v) FRAGMENT TYPE: -N Terminal fragment

315 (vi) ORIGINAL SOURCE:

316 (A) ORGANISM: Neisseria meningitidis

317 (B) STRAIN: B:4:P1.15

319 (vii) IMMEDIATE SOURCE:

320 (A) LIBRARY: Genomic

321 (B) CLONE: P64K

323 (ix) FEATURE:

324 (A) NAME/KEY: 1577

326 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8 :

327 GATCCTGATA TCAAAT

16

329 (2) INFORMATION FOR SEQ ID NO: 9:

331 (i) SEQUENCE CHARACTERISTICS:

332 (A) LENGTH: 15 Amino acid residues

RAW SEQUENCE LISTING ERROR SUMMARY                    DATE: 03/19/2003  
PATENT APPLICATION: US/09/612,925D                    TIME: 11:57:42

Input Set : N:\Crf3\RULE60\09612925.raw.txt  
Output Set: N:\CRF4\03192003\I612925D.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:2; Line(s) 124  
Seq#:5; Line(s) 225,227  
Seq#:21; Line(s) 739,741,745,747,749

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/612,925D

DATE: 03/19/2003

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Input Set : N:\Crf3\RULE60\09612925.raw.txt

Output Set: N:\CRF4\03192003\I612925D.raw

L:36 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:37 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:43 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)  
L:71 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=1  
L:107 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=2  
L:141 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=3  
L:174 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=4  
L:246 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=6  
L:283 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=7  
L:313 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=8  
L:571 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]  
L:571 M:238 W: Alpha Fields not Ordered, Reordered [(D) TOPOLOGY:] of (2)(i)  
L:571 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=17  
L:571 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=17  
L:598 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]  
L:598 M:238 W: Alpha Fields not Ordered, Reordered [(D) TOPOLOGY:] of (2)(i)  
L:598 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=18  
L:598 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=18  
L:640 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]  
L:640 M:238 W: Alpha Fields not Ordered, Reordered [(D) TOPOLOGY:] of (2)(i)  
L:640 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=19  
L:640 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=19  
L:685 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]  
L:685 M:238 W: Alpha Fields not Ordered, Reordered [(D) TOPOLOGY:] of (2)(i)  
L:685 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=20  
L:685 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=20  
L:734 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]  
L:734 M:238 W: Alpha Fields not Ordered, Reordered [(D) TOPOLOGY:] of (2)(i)  
L:734 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=21  
L:734 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=21